RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/791,017_
Source: _/FWO -_
Date Processed by STIC: _3/11/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	**SUGGESTED CORRECTION**

SERIAL NUMBER: _10/791, 017_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES) — Sequence(s) _____ missing. If **intentional,** please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING   DATE: 03/11/2004
PATENT APPLICATION: US/10/791,017   TIME: 08:20:42

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03112004\J791017.raw**

```
   5 <110> APPLICANT: JENAPHARM GmbH & Co. KG
   7 <120> TITLE OF INVENTION: Methods for Determining Hormonal Effects of Substances
   9 <130> FILE REFERENCE: Pat 3684/11
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/791,017
C--> 12 <141> CURRENT FILING DATE: 2004-03-02
  14 <160> NUMBER OF SEQ ID NOS: 7
  16 <170> SOFTWARE: PatentIn Ver. 2.1
```

The types of errors shown exist throughout the Sequence Listing. Please check all sequences for similar errors.

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

```
  376 <210> SEQ ID NO: 6
  377 <211> LENGTH: 33
  378 <212> TYPE: DNA
  379 <213> ORGANISM: synthetic
W--> 381 <220> FEATURE: Primer
W--> 382 <400> SEQUENCE: 6
E--> 383 gggaattctg cggggtctct gcatctagta ggg
  386 <210> SEQ ID NO: 7
  387 <211> LENGTH: 18
  388 <212> TYPE: DNA
  389 <213> ORGANISM: synthetic
W--> 391 <220> FEATURE: Primer
W--> 392 <400> SEQUENCE: 7
E--> 393 gcttgggtgg tcatatgg
```

invalid <213> response - See item 10 on Error Summary Sheet

never insert a response to <220>. Move response to <223> line

> <223>

69 33

invalid

move "primer" to <223> line

> <223> <

17 18

1) <220> is a "header" only. It never has a response. Explanatory material goes on <223> line. This error appears in most of the sequences

2) Invalid <213> responses are shown in sequences 3 through 7

VERIFICATION SUMMARY   DATE: 03/11/2004
PATENT APPLICATION: US/10/791,017   TIME: 08:20:43

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\03112004\J791017.raw**

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:351 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:352 M:283 W: Missing Blank Line separator, <400> field identifier
L:361 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:362 M:283 W: Missing Blank Line separator, <400> field identifier
L:371 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:372 M:283 W: Missing Blank Line separator, <400> field identifier
L:381 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:382 M:283 W: Missing Blank Line separator, <400> field identifier
L:383 M:254 E: No. of Bases conflict, LENGTH:Input:69 Counted:33 SEQ:6
L:391 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:392 M:283 W: Missing Blank Line separator, <400> field identifier
L:393 M:254 E: No. of Bases conflict, LENGTH:Input:17 Counted:18 SEQ:7